



- 34 -

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: NeuTec Pharma plc
- (B) STREET: Clinical Sciences Building, Central
Manchester Healthcare
- (C) CITY: Trust, Oxford Road, Manchester
- (E) COUNTRY: GB
- (F) POSTAL CODE (ZIP): M13 9WL

(ii) TITLE OF INVENTION: Treatment and Diagnosis of Infections of
Gram

Positive Cocci

(iii) NUMBER OF SEQUENCES: 15

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(vi) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: GB 9614274.0
- (B) FILING DATE: 06-JUL-1996

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 540 base pairs
- (B) TYPE: nucleic acid

- 35 -

(C) STRANDEDNESS: double

(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

ATGGTGGATT GGTATGGAC ATCCGTTTGG AACAGTAGAT TCACTTATCA GCCGAATACA
60
CCATTTGAAC AAAGAGCCTT ATTTGACATC AATAAGAAGA TCAAAGGAAA CAGTTATACT
120
GCATTAGTAG GGCATACCGG AAGCGGGAAA TCAACCTTAC TTCAGCATTG GAATGCGCTT
180
GTTAAGCCAA CAAGCGGTAC AGTCCATATT GGAGAACGAG ATATTCAGCC GGATACGGAT
240
AATAAGAATT TAAAGCCCAT CCGAAAAAAA GTTGGCATCG TCTTTCAGTT TCCAGAAGCA
300
CAGCTATTTCG AAGAAACGGT AGCAAAAGAC ATTGCTTTTCG GTCCTAAAAA CTTTGGTGTC
360
AGCGAAGAAG AAGCACTAGT CCTAGCAAAA GAAACATTAG AACAAGTTGG GCTGGATGAA
420
AGCTATTTGG AACGTTTCGCC ATTTGAACTT TCAGGAGGGC AAATGCGTAG AGTAGCAATC
480
GCTGGTGTGC TTGCCATGAG GCCGGAAGTA CTTGTATTGG ATGAACCAAC GGCAGGACTT
540

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

- 36 -

Met Val Asp Trp Leu Trp Thr Ser Val Leu Asn Ser Arg Phe Thr Tyr
 1 5 10 15

Gln Pro Asn Thr Pro Phe Glu Gln Arg Ala Leu Phe Asp Ile Asn Lys
 20 25 30

Lys Ile Lys Gly Asn Ser Tyr Thr Ala Leu Val Gly His Thr Gly Ser
 35 40 45

Gly Lys Ser Thr Leu Leu Gln His Leu Asn Ala Leu Val Lys Pro Thr
 50 55 60

Ser Gly Thr Val His Ile Gly Glu Arg Asp Ile Gln Pro Asp Thr Asp
 65 70 75 80

Asn Lys Asn Leu Lys Pro Ile Arg Lys Lys Val Gly Ile Val Phe Gln
 85 90 95

Phe Pro Glu Ala Gln Leu Phe Glu Glu Thr Val Ala Lys Asp Ile Ala
 100 105 110

Phe Gly Pro Lys Asn Phe Gly Val Ser Glu Glu Glu Ala Leu Val Leu
 115 120 125

Ala Lys Glu Thr Leu Glu Gln Val Gly Leu Asp Glu Ser Tyr Leu Glu
 130 135 140

Arg Ser Pro Phe Glu Leu Ser Gly Gly Gln Met Arg Arg Val Ala Ile
 145 150 155 160

Ala Gly Val Leu Ala Met Arg Pro Glu Val Leu Val Leu Asp Glu Pro
 165 170 175

Thr Ala Gly Leu

- 37 -

180

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Xaa Gly Xaa Gly Lys Ser Thr

1

5

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Thr Gly Ser Gly Lys Ser Thr

1

5

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids

(B) TYPE: amino acid

- 39 -

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Arg Val Ala Ile Ala Gly Val Leu

1

5

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1457 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

ATTTAAAGAA ATTATTAATA AAAAAATTGA ATTAGGATGT ACAGCTATGG CCATTTTTAA

60

ATATATAGAG AAAAAGGGTT ATGAAGGTAA ATATACTATT CTACGAGAAT ACTGTAAAAA

120

TAAAAAACAA AATGAGACTA AAAAAGCAAC TATACGCGTA GAACTAATC CCGGTATAGC

180

TGCTCAAGTA GACTGGAAAG AAGATATGGT AATGCATGAT AAGTTTGGCA GAACTTATCA

240

ATTCAACATC TTTCTTTACG TTCTACACTA TTCAAAAATG AAGTATATCA CATTAACTTG

300

- 40 -

GGATAGAAAA CAAGATACCT TATTGAATG TTTAAAAGAC GCTTTTGAAT ACACCGAAGG
360

GGTTCCAAAA GAAATCTGGT TCGATAATAT GAGAACTGTA GTTGATCGAC CTAGAACACA
420

ATATAAAAAA GTCGTCTTTA ATAATTTATT TTATCAATTT AGTAAGGATG CCAACTTTGA
480

ACCTATTGCT TGTAGACCCT ATCGTCCTCA AACAAAAGGG TCTGTTGAAT CATTAGCTAA
540

ATTTGTTGAA CAGCGTTTAA GACCATACGA TTATGAATTT TATGATGCTG TAGAACTTAT
600

TGGGCTAGTA AACGATTTAT GTCACGAATT GAATCACTTA GAAATTTTAC AAGCAACAGA
660

ACAACGACCT ATCGACGTTT TCAATTATGA AGAAAAAGAA CATTTAAATT CTTTTAATGC
720

CAAGTTACTA GATACTTACA TCGAAAATGA GTGTATAAGA ATCGTTTCTA AAGAATCGAT
780

GATTAACTTT AGAAAAGGTA AATACTCGGT ACCTACTAAA TACATTGGTG AAGAAGTACA
840

AGTGATATTC AATAATTCTA CTGATGAATT GCTGATTTAT TATGATGGTG AATTAATAAG
900

ACGGCATAAT CTATCCGAAA GAAAATTTAA TTATATCGTT GAAGATATGA GTGAAATATT
960

AAAATCAGAT GTATTTAAAC ATAAGGATGA CAAAGAAATT CTTACGTATA TAGAAAATTC
1020

ATTATTACTG TATGACGAAA TTAGGAGGA CTTTCGATGA ATACGAACCA TCAAAAATTA
1080

CTTAATAACT TTGAAATATT AAAACTAAAA AAATTCAAAG ATTATTATCC AACTATATT
1140

GAATTACTTT CTAAAAATGA GAAATCTTTA ACTGAAATAT TGATTGATTT AACGGAAAAA
1200

GAAATAGAAT ATCAATCAGA ATTAAATTT AAACGTGCTG TGAATTCAGC ACGTTTCCCT
1260

AAAATAAAAT ATTTACATGA TTTTGATTTT ATGTTTCAAC CTAAGTATAA ATCAACAAGA
1320

- 41 -

AATACTCACT TTAAATCTA TGCATTTTTT AGAAGATAGT ATAAATATTT GTTTCTAGTA
 1380
 ATAGTGGTGT TGGTAAACA CACCTAGCAA TCTCATTAGG AATAGAGGCA TGTTAGCAAA
 1440
 ATATAAAGAC TAGATCC
 1457

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Phe Lys Glu Ile Ile Asn Lys Lys Ile Glu Leu Gly Cys Thr Ala Met
 1 5 10 15

Ala Ile Phe Lys Tyr Ile Glu Lys Lys Gly Tyr Glu Gly Lys Tyr Thr
 20 25 30

Ile Leu Arg Glu Tyr Cys Lys Asn Lys Lys Gln Asn Glu Thr Lys Lys
 35 40 45

Ala Thr Ile Arg Val Glu Thr Asn Pro Gly Ile Ala Ala Gln Val Asp
 50 55 60

Trp Lys Glu Asp Met Val Met His Asp Lys Phe Gly Arg Thr Tyr Gln
 65 70 75 80

Phe Asn Ile Phe Leu Tyr Val Leu His Tyr Ser Lys Met Lys Tyr Ile

- 42 -

	85		90		95
Thr Leu Thr Trp Asp Arg Lys Gln Asp Thr Leu Phe Glu Cys Leu Lys					
	100		105		110
Asp Ala Phe Glu Tyr Thr Glu Gly Val Pro Lys Glu Ile Trp Phe Asp					
	115		120		125
Asn Met Arg Thr Val Val Asp Arg Pro Arg Thr Gln Tyr Lys Lys Val					
	130		135		140
Val Phe Asn Asn Leu Phe Tyr Gln Phe Ser Lys Asp Ala Asn Phe Glu					
145		150		155	160
Pro Ile Ala Cys Arg Pro Tyr Arg Pro Gln Thr Lys Gly Ser Val Glu					
	165		170		175
Ser Leu Ala Lys Phe Val Glu Gln Arg Leu Arg Pro Tyr Asp Tyr Glu					
	180		185		190
Phe Tyr Asp Ala Val Glu Leu Ile Gly Leu Val Asn Asp Leu Cys His					
	195		200		205
Glu Leu Asn His Leu Glu Ile Ser Gln Ala Thr Glu Gln Arg Pro Ile					
	210		215		220
Asp Val Phe Asn Tyr Glu Glu Lys Glu His Leu Asn Ser Phe Asn Ala					
225		230		235	240
Lys Leu Leu Asp Thr Tyr Ile Glu Asn Glu Cys Ile Arg Ile Val Ser					
	245		250		255
Lys Glu Ser Met Ile Asn Phe Arg Lys Gly Lys Tyr Ser Val Pro Thr					

- 43 -

260 265 270

Lys Tyr Ile Gly Glu Glu Val Gln Val Ile Phe Asn Asn Ser Thr Asp

275 280 285

Glu Leu Leu Ile Tyr Tyr Asp Gly Glu Leu Ile Arg Arg His Asn Leu
290 295 300

Ser Glu Arg Lys Phe Asn Tyr Ile Val Glu Asp Met Ser Glu Ile Leu
305 310 315 320

Lys Ser Asp Val Phe Lys His Lys Asp Asp Lys Glu Ile Leu Thr Tyr
325 330 335

Ile Glu Asn Ser Leu Leu Leu Tyr Asp Glu Ile
340 345

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Met Asn Thr Asn His Gln Lys Leu Leu Asn Asn Phe Glu Ile Leu Lys
1 5 10 15

Leu Lys Lys Phe Lys Asp Tyr Tyr Pro Asn Tyr Ile Glu Leu Leu Ser
20 25 30

Lys Asn Glu Lys Ser Leu Thr Glu Ile Leu Ile Asp Leu Thr Glu Lys

- 44 -

35 40 45

Glu Ile Glu Tyr Gln Ser Glu Leu Lys Phe Lys Arg Ala Val Asn Ser
50 55 60

Ala Arg Phe Pro Lys Ile Lys Tyr Leu His Asp Phe Asp Phe Met Phe
65 70 75 80

Gln Pro Lys Tyr Lys Ser Thr Arg Asn Thr His Phe Lys Ile Tyr Ala
85 90 95

Phe Phe Arg Arg
100

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Ala Gln Val Asp Trp Lys Glu
1 5

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

- 45 -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

Ala Phe Glu Tyr Thr Glu Gly Val Pro Lys

1

5

10

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Thr Lys Ser Gly Val Glu

1

5

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

Ser Gly Val Gly Lys Thr His Leu Ala

1

5